

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(i) APPLICANT: DUAN, ROXANNE
RUBEN, STEVEN

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(ii) TITLE OF INVENTION: Parotid Secretory Protein

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(iii) NUMBER OF SEQUENCES: 18

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(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: HUMAN GENOME SCIENCES, INC.
(B) STREET: 9410 KEY WEST AVENUE
(C) CITY: ROCKVILLE
(D) STATE: MD
(E) COUNTRY: US
(F) ZIP: 20850

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

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(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:

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(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: BROOKES, ANDERS A.
(B) REGISTRATION NUMBER: 36,373
(C) REFERENCE/DOCKET NUMBER: PF348

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(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1028 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

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(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 49..795

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(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 49..100

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(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 103..795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CACGAGATT CATGAGCATC CTCCCTCTAAA CGCGTGTCAA GACAAAAG ATG CTT CAG
Met Leu Gln

5	CTT TGG AAA CTT GTT CTC CTG TGC GGC GTG CTC ACT GGG ACC TCA GAG Leu Trp Lys Leu Val Leu Leu Cys Gly Val Leu Thr Gly Thr Ser Glu -15 -10 -5 1	105
10	TCT CTT CTT GAC AAT CTT GGC AAT GAC CTA AGC AAT GTC GTG GAT AAG Ser Leu Leu Asp Asn Leu Gly Asn Asp Leu Ser Asn Val Val Asp Lys 5 10 15	153
15	CTG GAA CCT GTT CTT CAC GAG GGA CTT GAG ACA GTT GAC AAT ACT CTT Leu Glu Pro Val Leu His Glu Gly Leu Glu Thr Val Asp Asn Thr Leu 20 25 30	201
20	AAA GGC ATC CTT GAG AAA CTG AAG GTC GAC CTA GGA GTG CTT CAG AAA Lys Gly Ile Leu Glu Lys Leu Lys Val Asp Leu Gly Val Leu Gln Lys 35 40 45	249
25	TCC AGT GCT TGG CAA CTG GCC AAG CAG AAG GCC CAG GAA GCT GAG AAA Ser Ser Ala Trp Gln Leu Ala Lys Gln Lys Ala Gln Glu Ala Glu Lys 50 55 60 65	297
30	TTG CTG AAC AAT GTG ATT TCT AAG CTG CTT CCA ACT AAC ACG GAC ATT Leu Leu Asn Asn Val Ile Ser Lys Leu Leu Pro Thr Asn Thr Asp Ile 70 75 80	345
35	TTT GGG TTG AAA ATC AGC AAC TCC CTC ATC CTG GAT GTC AAA GCT GAA Phe Gly Leu Lys Ile Ser Asn Ser Leu Ile Leu Asp Val Lys Ala Glu 85 90 95	393
40	CCG ATC GAT GAT GGC AAA GGC CTT AAC CTG AGC TTC CCT GTC ACC GCG Pro Ile Asp Asp Gly Lys Gly Leu Asn Leu Ser Phe Pro Val Thr Ala 100 105 110	441
45	AAT GTC ACT GTG GCC GGG CCC ATC ATT GGC CAG ATT ATC AAC CTG AAA Asn Val Thr Val Ala Gly Pro Ile Ile Gly Gln Ile Ile Asn Leu Lys 115 120 125	489
50	GCC TCC TTG GAC CTC CTG ACC GCA GTC ACA ATT GAA ACT GAT CCC CAG Ala Ser Leu Asp Leu Leu Thr Ala Val Thr Ile Glu Thr Asp Pro Gln 130 135 140 145	537
55	AGA CAC CAG CCT GTT GCC GTC CTG GGA GAA TGC GCC AGT GAC CCA ACC Thr His Gln Pro Val Ala Val Leu Gly Glu Cys Ala Ser Asp Pro Thr 150 155 160	585
60	AGC ATC TCA CTT TCC TTG CTG GAC AAA CAC AGC CAA ATC ATC AAC AAG Ser Ile Ser Leu Ser Leu Asp Lys His Ser Gln Ile Ile Asn Lys 165 170 175	633
65	TTC GTG AAT AGC GTG ATC AAC ACG CTG AAA AGC ACT GTA TCC TCC CTG Phe Val Asn Ser Val Ile Asn Thr Leu Lys Ser Thr Val Ser Ser Leu 180 185 190	681
70	CTG CAG AAG GAG ATA TGT CCA CTG ATC CGC ATC TTC ATC CAC TCC CTG Leu Gln Lys Glu Ile Cys Pro Leu Ile Arg Ile Phe Ile His Ser Leu 195 200 205	729
75	GAT GTG AAT GTC ATT CAG CAG GTC GTC GAT AAT CCT CAG CAC AAA ACC Asp Val Asn Val Ile Gln Gln Val Val Asp Asn Pro Gln His Lys Thr 210 215 220 225	777
80	CAG CTG CAA ACC CTC ATT TGAAGAGGAC GAATGAGGAG GACCACTGTG Gln Leu Gln Thr Leu Ile 230	825
85	GTGCATGCTG ATTGGTCCCC AGTGGCTTGC CCCACCCCC TATAGCATCT CCCTCCAGGA AGCTGCTGCC ACCACCTAAC CAGCGTGAAA GCCTGAGTCC CACCAAGG ACCTTCCCAG	885
90		945

ATACCCCTTC TCCTCACAGT CAGAACAGCA GCCTCTACAC ATGTTGTCCT GCCCCTGGCA 1005
 ATAAAGGCC ATTCTGCAA AAA 1028

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(2) INFORMATION FOR SEQ ID NO:2:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 249 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Leu Gln Leu Trp Lys Leu Val Leu Leu Cys Gly Val Leu Thr Gly
 18 -15 -10 -5

20 Thr Ser Glu Ser Leu Leu Asp Asn Leu Gly Asn Asp Leu Ser Asn Val
 1 5 10
 Val Asp Lys Leu Glu Pro Val Leu His Glu Gly Leu Glu Thr Val Asp
 15 20 25 30

25 Asn Thr Leu Lys Gly Ile Leu Glu Lys Leu Lys Val Asp Leu Gly Val
 35 40 45

30 Leu Gln Lys Ser Ser Ala Trp Gln Leu Ala Lys Gln Lys Ala Gln Glu
 50 55 60

Ala Glu Lys Leu Leu Asn Asn Val Ile Ser Lys Leu Leu Pro Thr Asn
 65 70 75

35 Thr Asp Ile Phe Gly Leu Lys Ile Ser Asn Ser Leu Ile Leu Asp Val
 80 85 90

40 Lys Ala Glu Pro Ile Asp Asp Gly Lys Gly Leu Asn Leu Ser Phe Pro
 95 100 105 110

Val Thr Ala Asn Val Thr Val Ala Gly Pro Ile Ile Gly Gln Ile Ile
 115 120 125

45 Asn Leu Lys Ala Ser Leu Asp Leu Leu Thr Ala Val Thr Ile Glu Thr
 130 135 140

Asp Pro Gln Thr His Gln Pro Val Ala Val Leu Gly Glu Cys Ala Ser
 145 150 155

50 Asp Pro Thr Ser Ile Ser Leu Ser Leu Leu Asp Lys His Ser Gln Ile
 160 165 170

Ile Asn Lys Phe Val Asn Ser Val Ile Asn Thr Leu Lys Ser Thr Val
 175 180 185 190

55 Ser Ser Leu Leu Gln Lys Glu Ile Cys Pro Leu Ile Arg Ile Phe Ile
 195 200 205

60 His Ser Leu Asp Val Asn Val Ile Gln Gln Val Val Asp Asn Pro Gln
 210 215 220

His Lys Thr Gln Leu Gln Thr Leu Ile
 225 230

65 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 235 amino acids
 (B) TYPE: amino acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Phe Gln Leu Gly Ser Leu Val Val Leu Cys Gly Leu Leu Ile Gly
 1 5 10 15

Asn Ser Glu Ser Leu Leu Gly Glu Leu Gly Ser Ala Val Asn Asn Leu
 15 20 25 30

Lys Ile Leu Asn Pro Pro Ser Glu Ala Val Pro Gln Asn Leu Asn Leu
 35 40 45

Asp Val Glu Leu Leu Gln Gln Ala Thr Ser Trp Pro Leu Ala Lys Asn
 20 50 55 60

Ser Ile Leu Glu Thr Leu Asn Thr Ala Asp Leu Gly Asn Leu Lys Ser
 25 65 70 75 80

Phe Thr Ser Leu Asn Gly Leu Leu Lys Ile Asn Asn Leu Lys Val
 85 90 95

Leu Asp Phe Gln Ala Lys Leu Ser Ser Asn Gly Asn Gly Ile Asp Leu
 30 100 105 110

Thr Val Pro Leu Ala Gly Glu Ala Ser Leu Val Leu Pro Phe Ile Gly
 115 120 125

Lys Thr Val Asp Ile Ser Val Ser Leu Asp Leu Ile Asn Ser Leu Ser
 35 130 135 140

Ile Lys Thr Asn Ala Gln Thr Gly Leu Pro Glu Val Thr Ile Gly Lys
 40 145 150 155 160

Cys Ser Ser Asn Thr Asp Lys Ile Ser Ile Ser Leu Leu Gly Arg Arg
 165 170 175

Leu Pro Ile Ile Asn Ser Ile Leu Asp Gly Val Ser Thr Leu Leu Thr
 45 180 185 190

Ser Thr Leu Ser Thr Val Leu Gln Asn Phe Leu Cys Pro Leu Leu Gln
 195 200 205

Tyr Val Leu Ser Thr Leu Asn Pro Ser Val Leu Gln Gly Leu Leu Ser
 50 210 215 220

Asn Leu Leu Ala Gly Gln Val Gln Leu Ala Leu
 55 225 230 235

60 (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 235 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

65 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Phe Gln Leu Gly Ser Leu Val Val Leu Cys Gly Leu Leu Ile Gly
 1 5 10 15

5 Thr Ser Glu Ser Leu Leu Gly Asp Val Ala Asn Ala Val Asn Asn Leu
 20 25 30

10 Asp Ile Leu Asn Ser Pro Ser Glu Ala Val Ala Gln Asn Leu Asn Leu
 35 40 45

15 Asp Val Gly Ser Leu Gln Gln Ala Thr Thr Trp Pro Ser Ala Lys Asp
 50 55 60

20 Ser Ile Leu Glu Thr Leu Asn Lys Val Glu Leu Gly Asn Ser Asn Gly
 65 70 75 80

25 Phe Thr Pro Leu Asn Gly Leu Leu Leu Arg Val Asn Lys Phe Arg Val
 85 90 95

30 Leu Asp Leu Gln Ala Gly Leu Ser Ser Asn Gly Lys Asp Ile Asp Leu
 100 105 110

35 Lys Leu Pro Leu Val Phe Glu Ile Ser Phe Ser Leu Pro Val Ile Gly
 115 120 125

40 Pro Thr Leu Asp Val Ala Val Ser Leu Asp Leu Leu Asn Ser Val Ser
 130 135 140

45 Val Gln Thr Asn Ala Gln Thr Gly Leu Pro Gly Val Thr Leu Gly Lys
 145 150 155 160

50 Cys Ser Gly Asn Thr Asp Lys Ile Ser Ile Ser Leu Leu Gly Arg Arg
 165 170 175

55 Leu Pro Phe Val Asn Arg Ile Leu Asp Gly Val Ser Gly Leu Leu Thr
 180 185 190

60 Gly Ala Val Ser Ile Leu Leu Gln Asn Ile Leu Cys Pro Val Leu Gln
 195 200 205

65 Tyr Leu Leu Ser Thr Met Ser Gly Ser Ala Ile Gln Gly Leu Leu Ser
 210 215 220

70 Asn Val Leu Thr Gly Gln Leu Ala Val Pro Leu
 225 230 235

(2) INFORMATION FOR SEQ ID NO:5:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 206 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: protein

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Phe Gln Leu Gly Ser Leu Val Val Leu Cys Gly Leu Leu Ile Gly
 1 5 10 15

65 Thr Ser Gly Ser Leu Phe Asp Ile Phe Gln Asn Pro Glu Leu Asp Val
 20 25 30

Glu Ser Val Trp Ser Glu Ile Asn Tyr Arg Ile Arg Tyr Ala Leu Glu
 35 40 45

5	Thr	Met	Asp	Leu	Asp	Met	Leu	Ala	Asp	Tyr	Leu	Ser	Lys	Arg	Gly	Ile
	50						55					60				
10	Glu	Leu	Lys	Ile	Lys	Asp	Leu	Arg	Ile	Leu	Asn	Leu	Asn	His	Glu	Val
	65					70				75				80		
15	Ser	Pro	Asn	Gly	Asp	Glu	Val	Thr	Leu	Lys	Met	Pro	Met	Ala	Leu	Asn
					85				90					95		
20	Ala	Ser	Leu	Ser	Leu	Pro	Ala	Arg	Asp	Leu	Thr	Thr	Asp	Val	Ser	Ile
					100				105					110		
25	Ser	Met	Glu	Ala	Ile	Thr	Ser	Phe	Ala	Ile	Glu	Lys	Asp	Pro	Lys	Thr
		115						120					125			
30	Gly	Arg	Arg	Val	Leu	Asn	Met	Gln	Arg	Cys	Ser	Leu	Asn	Thr	Asp	Asn
				130				135					140			
35	Thr	Ser	Ile	Ser	Leu	Leu	Asn	Arg	Lys	Ser	Asn	Phe	Val	Asn	Leu	Ala
				145				150					155		160	
40	Leu	Asp	Ser	Ala	Leu	Tyr	Leu	Ile	Lys	Arg	Gly	Leu	Thr	Leu	Pro	Val
					165				170					175		
45	Arg	Arg	Gln	Leu	Cys	Pro	Val	Leu	Gln	Leu	Ile	Ile	Ser	Asn	Thr	Phe
					180				185					190		
50	His	Pro	Asp	Glu	Ile	Ser	Asn	Pro	Gln	Thr	Ala	Ile	Ser	Thr		
					195				200					205		

(2) INFORMATION FOR SEQ ID NO:6:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTACAGCCAT GGAGTCTCTT CCTGACAATC TTGGCAATG

(2) INFORMATION FOR SEQ ID NO:7:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

60

ATTCACCTT CCTTCAGCCG TTTCGACCTG CCTTTT

65 (2) INFORMATION FOR SEO ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

10 CTACGCGGAT CCGCCATCAT GCTTCAGCTT TGGAAACTTG TTC

43

(2) INFORMATION FOR SEQ ID NO:9:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

30 CTCTGCTCTA GACTAAATGA GGGTTTGCAG C

31

(2) INFORMATION FOR SEQ ID NO:10:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 449 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

45 GGCACGAGAT TTCATGAGCA TCCTCCTCTA AACGCGTGTC AAGACAAAAG ATGCTTCAGC

60

TTTGGAAACT TGTCTCCTG TGCGGCGTGC TCACTGGAC CTCAGAGTCT CTTCTTGACA

120

50 ATCTTGGCAA TGACCTAAGC AATGTCGTGG ATAAGCTGGA ACCTGTTCTT CACGAGGGAC

180

TTGAGACAGT TGACAATACT CTTAAAGGGC ATCCCCNTTT TNGAGAAACT GAAGGTCGAC

240

CTAGGAGTGC TTCAGAAATC CAGTGTTGG CAACTGGCCA AGCAGAAGGC CCAGGAAGCT

300

55 GAGAAATTGC TGAACCAATG TCATTTCTAA GCTGCTTCCA ACTAACACGG ACATTTTTGG
 GGTAAAAAT CAGCAACTCC CTCATCCTGG ATGTCAAAGC TGAACCGATC GATGATGGNA

360

420

AAGGCTTAAA CTGGAGCTTC CCTGTCANC

449

60 (2) INFORMATION FOR SEQ ID NO:11:

65 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 538 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

5 ATGAGCATCC TCCTCTAACG CGGTGTCAAG ACAAAAGATG CTNNCAGCTT TGGAAACTTG 60
 TTCTCCTGTG CGGGGTGCTC ACTGGGACCT CAGAGTCTCT TCTTGACAAT CTTGGCAATG 120
 10 ACCTAAGCAA TGTCTGGAT AAGCTGGAAC CTGTTCTTCA CGAGGGACTT GAGACAGTTG 180
 ACAATACTCT TAAAGGCATC CTTGAGAAC TGAAGGTCGA CCTAGGAGTG CTTCAGAAAT 240
 15 CCAGTGCTTG GCAACTGGCC AACAGAAGGN CCAGGAAGCT GAGAAATTGC TGAACAATGT 300
 CATTCTAAG CTGCTTCAA CTAACACGG AATTTTGGG TTGAAANTCA GCAATNCCCN 360
 CANCCGGATG TTCAAAGNTG NANCGATCGA TGATGGGAA AGGCTTAAAN CCGGAGGCTT 420
 20 CCCTGTTAC CGGGAAATGTT CAANGTNGGC CCGGGCCNT CATTGGGCCA GNTTATCAAA 480
 NCTGGAAAGC TTCCCTGGGAC CTCCGGACNG GNTCAACAAT TGAAANGATT CCCCAGA 538

(2) INFORMATION FOR SEQ ID NO:12:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 359 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic).

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

35 GGCACGAGAT TTCATGAGCA TCCTCCTCTA AACGCGTGTCAAG ACAAAAGATG ATGCTTCAGC 60
 40 TTTGGAAACT TGTTCTCCTG TGCGGGGTGTC TCACTGGGAC CTCAGAGTCT CTTCTTGACA 120
 ATCTTGCAA TGACCTAAGC AATGTCGTGG ATAAGCTGGG AACCTGTTCT TCACGAGGG 180
 45 CTTGAGACAG TTGACAATAC TCTTAAAGGC ATCCTTGAGA AACTGAAGGT CGANCTAGGA 240
 GTGCTTCAGA AATCCAGTGC TTGGCAACTG GNCAAGCAGA AGGNCCAGG AAGCTGAGAA 300
 ATTGCTGGAN CAATGTCAAT TCTAAGCTGN TTCCGACTAA CACGGNCATT TTTGGGTIG 359

(2) INFORMATION FOR SEQ ID NO:13:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 374 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 55 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic).

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

60 ACCCACCGCGT CGGGGTGAT CAACACGCTG AAAAGCACTG TATCCTCCCT GCTGCAGAAG 60
 GAGATATGTC CACTGATCCG CATCTTCATC CACTCCCTGG ATGTGAATGT CATTCAAGCAG 120
 GTCGTGATA ATCCTCAGCA CAAAACCCAG CTGCAAACCC TCATCTGAAG AGGACGAATG 180

	AGGAGGACCA CTGTGGTGCA TGCTGATTGG TTCCCAGTGG CTTGCCAAC CCCCTTATAG	240
5	CATCTCCCTC CAGGAAGCTG CTGCCACCAC CTAACCAGCG TGAAAGCCTG GAGTCCCACC	300
	AGAAGGACCT TCCCAGATAAC CCCTTTTCC TCACAGTCAG AGGNGNNNGC CTCTTACACN	360
	TGTTGTCCNG GCCC	374

10 (2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

25	TTCATGAGCA TCCTCCTCTA AACGCGTGTCA AAGACAAAAG ATGCTTCACT TTGGAAACTT	60
	GTTCTCTGTGCGCGTGTCT CACTGGGACC TCAGAGTCCTC TTCTTGACAA TCTTGGCAAT	120
30	GACCTAAGCA ATGTCGTGGA TAAGCTGGAA CCTGTTCTTC ACGAGGGACT TGAGACAGTT	180
	GACAATACTC TTAAAGGCAT CCTTGAGAAA CTGAAGGTGAC ACCTAGGAGT GCTTCAGAAA	240
	TCCAGTGCTT GGCAACTGGG CCANCAAGAAA GGCCCAGGGA AAGCGGAGAA ATTGCTGGAA	300
35	CAATGTTCAT TTCTAAAGCT GCTTCCAAC TAACACGGGA CNTTTTGGG GTTTGNAAAA	360
	TCAGCCAACT TCCCTCAACC NNGGATGTTCAAAAGCTGGAA AACCGN	406

40 (2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

55	TCGACCCACG CGTCCGCCGC CCCAACCTTT TTGGCAGTTC TCCCATCTCT TGCCCACCTTG	60
	ACAGACACTT AATAGTTCCC TGTGTTTCC AGACACAGCC AAATCATCAA CAAGTTCGTG	120
	AATAGCGTGA TCAACACGCT GAAAAGCACT GTATCCTCCC TGCTGCAGAA GGAGATATGT	180
60	CCACTGATCC GCATCTTCAT CCACTCCCTG GATGTGAATG TCATTTCAGCA GGTCGTCGAT	240
	AATCCTCAGC ACAAAACCA GCTGCAAACC CTCATCTGAA GAGGACGAAT GAGGAGGACC	300
	ACTGTGGTGC ATGCTGGTGA GGAGCCAGTC TCTGTGCCCA AATGCACAGG GGCCTATGGT	360
65	GAAGTAAAG TCAAGCGTGG CTTCCCTTAT TTTTGTGTTA GAAGACTGTG CCTTCATCTC	420
	AGTCATAGAT TGAGCCCTGG NCCCCATCCC ANGCTAAGGC CTGATTCTGG TCANACTCTG	480

AACACTGAGC CTT

493

(2) INFORMATION FOR SEQ ID NO:16:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 395 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TCGACCCACA CGTCCGCCTG ACTGACAGAA GGAGATATGT CCATGATCCG ACATTCTTAC	60
ATCCACTCCC TGGATGTGAA TGTTCAATTNC AGCAGGTCGT NCGATAATCC NGCAGCACAA	120
AACCCAGCTG GCAAACCCCTN CATCTGAAGA NGACGAATGA GGANGACCAC TGTGGGTGCA	180
TGCTGATTGG TNTCCCACTG GCCTTGCCCC AACCCCTTA NAGCANCTCC CTCCAGGAAG	240
25 CTGCTGCNAA CCAACCGAAC CAGCGTGAAA GCCTGAATNC CACCAGAAGG ACCTTCCCAG	300
ATANCCCTGC TNCNCAACAG TNAAGAACAG CAGCTTCGAA CAACATGNGG TTCTGGCCCC	360
CGGGCAATAA AAGGCCATT TTGGCAAAAA AAAAAA	395

30 (2) INFORMATION FOR SEQ ID NO:17:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 116 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: DNA (genomic)

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGCACCGANAT TTCACTGAGCA TCCTCCTCTA AACACGTGTC AAGACAAAAG ATGCTTCAGC	60
45 TTTGGNAACT TGTTCCTCTA TNCNGCGTGC TCACTGNAC CTCAGAAATCT CTNCTT	116

50 (2) INFORMATION FOR SEQ ID NO:18:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 360 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: DNA (genomic)

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GTGGNCCGGG GCCCATCATT GGGCCAGANT TATCAACCTG AAAGCCTCCN NGGANCTCCT	60
60 GACCGCAGTC AACAAATTGGA AACTGGATCC CCCAGAACAA CAACCAGCCT GGTTGNCCGT	120
NCTGGGAAG AATGCCNCC AATGAANCCC AAACCAAGCA NCTTCACTNN TNCCTNGGCT	180
65 GGGGACCAAA ACACCAGGCC AAAATCCANT NAANCAAGTN TCCGTGGNAA TAAGCGTGGA	240
ATCCAAACAA CGCTGGAAA AAGCANTGGG NATNCCNTCC CTGGCTGGGC AAGAAAGGGN	300
GATATGGTCC ACTGGAATCC GGAATTTTA ANCCAATTCC CTNGGAATGT GGNAATGTCA	360